

# A Bayesian Source Term inversion Method Based on Spatiotemporal Trajectory Prior and Joint Adaptive MCMC Sampling

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Determining the release source position and quantity is crucial for evaluating the consequences of atmospheric radionuclide release events, with the Bayesian method serving as the primary tool for source inversion. Reducing the impact of input data errors on inversion uncertainty and improving computational efficiency are key to developing robust and efficient inversion algorithms. To address these challenges, we developed a spatiotemporal trajectory prior (STP) distribution that effectively mitigates the influence of measurement and simulation errors on inversion results without increasing computational costs, thereby enhancing the robustness and accuracy of the inversion process. Additionally, we introduced a joint adaptive Markov Chain Monte Carlo (MCMC) sampling method that integrates the traditional parallel tempering (PT) algorithm with a novel joint adaptive transition proposal (JATP) algorithm to accelerate inversion calculations. The proposed methods were optimized and validated using data from the first release of the European Tracer Experiment (ETEX-I). After determining the hyperparameters, the JATP algorithm consistently maintained the sampling process near the theoretically optimal acceptance rate of 0.234. The PT algorithm, utilizing an optimized temperature schedule, achieved a 2.89-fold improvement in sampling efficiency compared to single-chain sampling. Under bootstrap statistical comparison, the method reduced the relative error of position, relative error of release quantity, and total relative error by 25.9%, 27.7%, and 27.8%, compared to the traditional uniform prior method, respectively. And the deviation of the estimated and true source position is within 0.25. The results demonstrate the accuracy and effectiveness of our method.

Keywords: Radionuclide source inversion. Spatiotemporal trajectory prior distribution. Joint adaptive transition proposal.

## I. INTRODUCTION

Environmental protection is a critical consideration in the development of the nuclear industry. Various stages, including the operation of nuclear power plants, isotope production, and the reprocessing of radioactive waste, involve environmental concerns related to the atmospheric release of radionuclides. Since the Chernobyl nuclear accident[1] and the Fukushima accident[2], this issue has garnered significant attention from both the academic community and the general public[3]. In recent years, several incidents involving radionuclide releases have further highlighted these concerns, including the abnormal detection of  $^{131}\text{I}$  in 2011[4], the  $^{106}\text{Ru}$  leak in 2017[5], and the detection of  $^{134}/^{137}\text{Cs}$  in 2020[6]. These events underscore the challenges of accurately predicting the dispersion of radioactive pollutants, primarily due to the lack of crucial source term information, such as the position, timing, and quantity of releases. This knowledge gap complicates the evaluation of accident consequences and hampers effective emergency response. Consequently, the accurate and timely inversion of source term information has become an essential priority[7, 8].

Methods for source inversion are generally divided into two categories: optimization methods and probabilistic modeling methods. Research on optimization methods[9–12] primarily focuses on enhancing cost function constraints through regularization techniques[13–15] and developing more efficient optimization algorithms[14, 16]. However,

these methods often struggle with accurately identifying the source position, prompting the integration of auxiliary positioning algorithms in some studies[17–20]. Probabilistic modeling methods, typically framed within Bayesian inference, construct the posterior distribution of source term parameters based on model-observation hypotheses[21, 22]. This approach provides statistically robust and interpretable results by delivering distributions of reconstructed parameters. Recent studies demonstrate the effectiveness of Bayesian methods in source inversion[23–29]. Nonetheless, most previous work has focused on designing likelihood functions using the L1 or L2 norm of the difference between simulated and observed detections, often overlooking the critical role of the prior function[23–26, 29]. This neglect limits the effective use of sparse detection data, exacerbating the inherent ill-posedness of inversion problems. Real-world scenarios further complicate this process, as detection data are often sparse and of varying quality. Additionally, inaccuracies in meteorological input fields and errors in dispersion model simulations can unpredictably affect inversion results, posing significant challenges to achieving robust source term estimates using Bayesian methods[7, 22]. Moreover, deriving accurate posterior distributions for source parameters frequently requires extensive iterative sampling, making computational efficiency a critical concern for Bayesian probabilistic modeling[30–32].

To address the limitations of traditional Bayesian methods in complex scenarios—namely, insufficient robustness, accuracy in source inversion, and slow computational speed—we propose an enhanced Bayesian framework that integrates the spatiotemporal trajectory prior (STP) distribution and a joint adaptive Markov Chain Monte Carlo (MCMC) sampling ap-

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60 approach for source inversion. The STP distribution is founded  
 61 on the principle that, for a single release source, all plumes  
 62 passing through detection points originate and overlap at the  
 63 source location. This provides a robust prior for source  
 64 term parameters, incorporating additional information be-  
 65 yond what L1 or L2 norm distributions can offer. Conse-  
 66 quently, it significantly improves the accuracy and robustness  
 67 of source inversion results. Moreover, the STP approach al-  
 68 lows for a rapid and reasonably accurate estimation of the  
 69 potential range of source term parameters prior to complex  
 70 iterative computations, making it broadly applicable to var-  
 71 ious inversion algorithms beyond the Bayesian framework.  
 72 To further enhance computational efficiency and ensure stable  
 73 convergence of MCMC sampling, we proposed a joint adap-  
 74 tive sampling method based on the classical parallel temper-  
 75 ing MCMC approach. This method combines the adaptability  
 76 of single adaptive transition proposals for high-dimensional  
 77 complex distributions with mechanisms to mitigate devia-  
 78 tions from Markovian properties during the sampling pro-  
 79 cess. As a result, it ensures efficient and reliable sampling  
 80 of high-dimensional distributions, addressing key challenges  
 81 in source inversion under complex conditions.

82 Using data from the first release of the European Tracer  
 83 Experiment (ETEX- I)[33], we designed three validation  
 84 schemes to optimize the hyperparameters of the proposed  
 85 method and validate its effectiveness, as well as its sensitivity  
 86 to input errors. In previous studies, researchers typically used  
 87 the data from fixed-sites to validate inversion methods[7, 29].  
 88 However, Xu et al.[7] highlight that the choice of sites has  
 89 a significant impact on inversion results. Therefore, we em-  
 90 ployed the bootstrap method[34] to statistically evaluate the  
 91 properties of the proposed method, providing a robust valida-  
 92 tion framework.

## II. MATERIALS AND METHODS

94 This section first presents the modeling approach for the at-  
 95 mospheric radionuclide release source inversion problem. It  
 96 then introduces the construction of the STP function and like-  
 97 lihood function within the Bayesian framework, followed by  
 98 a discussion on the joint adaptive MCMC sampling method.  
 99 Finally, the section describes the validation benchmarks and  
 100 evaluation metrics for the proposed method.

### A. Modeling

102 When solving inversion problems, we typically know the  
 103 detection vector  $\mathbf{Y}$ , and attempt to solve for the release vec-  
 104 tor  $\mathbf{X}$ . Inverse modeling usually assumes that these vectors  
 105 satisfy a mapping relationship,

$$106 \quad \mathbf{Y} = \mathbf{H}\mathbf{X} + \boldsymbol{\varepsilon} \quad (1)$$

107 Where  $\mathbf{H}$  is denoted as the source-receptor sensitivity matrix,  
 108 hereafter referred to as SRSM, and  $\boldsymbol{\varepsilon}$  represents the possi-  
 109 ble error vector, which is explained in more detail in relevant  
 110 study[35].

111 In this paper, the release time of release source is consid-  
 112 ered, as it is usually unknown in most cases that require es-  
 113 timation. In inversion efforts involving unknown position re-  
 114 lease source, it is common practice to assume that the source  
 115 is a homogeneous release at a specific point in time to re-  
 116 duce the dimensionality of the solution space[7, 16, 36], i.e.,  
 117 the source term is fully characterized by parameter  $\mathbf{X} =$   
 118  $[\mathbf{x}, t_s, t_e, Q]$ , where  $\mathbf{x} = (x_{lon}, x_{lat})$  represents coordinates  
 119 of source release position, and  $t_s$ ,  $t_e$  and  $Q$  represent the start  
 120 time, end time, and total release of the release source, respec-  
 121 tively. Thus, eq.1 can be expressed as:

$$122 \quad y_j = \hat{y}_j + \varepsilon_j \\ = \sum_k h_{jk}(\mathbf{x}_i) \frac{Q\Delta t_k}{t_e - t_s} + \varepsilon_j \quad (2)$$

123 where,  $h$  represents the elements in the transfer matrix  $\mathbf{H}$ ,  
 124  $j = 1 \dots m$  with  $m$  is the number of receptor samples,  
 125  $i = 1 \dots n$  with  $n$  represents the number of possible release  
 126 positions and  $k = 1 \dots l$ , where  $k$  denotes the number of  
 127 discrete intervals ( $\Delta t_k$ ) between  $t_s$  and  $t_e$ . The error between  
 128 detected data  $y_j$  and simulated data  $\hat{y}_j$  is denoted as  $\varepsilon_j$ , which  
 129 includes both measurement error and simulation error. It is  
 130 often difficult to assess this error in practice, so we estimate  
 131 the covariance matrix  $\mathbf{R}$  of the detected and simulated datas  
 132 as an unknown parameter in the source term inversion, i.e.,  
 133  $\mathbf{X} = [\mathbf{x}, t_s, t_e, Q, \mathbf{R}]$ .

134 The source-receptor sensitivity matrix (SRSM) describes  
 135 the sensitivity of observations with respect to the unit release.  
 136 Rajaona et al. [37] noted that this is the most time-consuming  
 137 step in the inversion algorithm. Fortunately, the adjoint-based  
 138 backward dispersion computation addresses this issue and has  
 139 been demonstrated by Seibert et al. [38] to be equivalent to  
 140 forward dispersion. In source term inversion problems with  
 141 unknown position, the number of receptor points is signifi-  
 142 cantly smaller than the potential source positions, making it  
 143 well-suited for calculating the SRSM matrix through back-  
 144 ward dispersion[39]. In this work, we perform dispersion cal-  
 145 culations using the backward mode of the Lagrangian Particle  
 146 Dispersion Model (LPDM) FLEXPART [40].

### B. Probabilistic description

148 The implementation of the Bayesian inversion algorithm  
 149 relies on the application of Bayes' rule:

$$150 \quad p(x|y) = \frac{p(y|x)p(x)}{p(y)} \propto p(y|x)p(x) \quad (3)$$

151 with the objective of obtaining the posterior distribution  
 152  $p(x|y)$  for the scenario by estimating a reasonable likelihood  
 153 function  $p(y|x)$  and prior distribution  $p(x)$ . Constructing the  
 154 posterior probability density function is crucial for the accu-  
 155 racy of source term inversion. A well-designed construction  
 156 ensures that the inferred distribution of source parameters in  
 157 complex scenarios aligns more closely with the true source  
 158 term.

159      *1. Prior distribution of variables*

160    It is common practice to assume that the variables are inde-  
 161    pendent of one other in sampling or fitting algorithms for mul-  
 162    tivariate coupled complex probability density function[23–  
 163    29]. Under this assumption we set priors for each variable  
 164    separately and define the product as the total prior:

165     $P(\mathbf{X}) = P(\mathbf{x}_i) \cdot P(t_s) \cdot P(t_e) \cdot P(Q) \cdot P(\mathbf{R})$  (4)

166    In almost all previous work, the prior probability density  
 167    functions for release location and time were chosen as uni-  
 168    form distributions over the range of possibilities due to  
 169    the lack of prior knowledge[23–26, 29, 41–43]. Inspired  
 170    by previous studies[15, 18], we have developed a back-  
 171    ward trajectory-based computation of spatiotemporal prior  
 172    distributions, which provides prior information that has not  
 173    been utilized in previous probabilistic modeling algorithms,  
 174    thereby enabling a more accurate estimation of the source  
 175    term.

176    As mentioned in section II A, SRSM is computed in this  
 177    work using the backward dispersion model. This calculation  
 178    incorporates the backward dispersion trajectory information  
 179    with the receptor points serving as the source, which is re-  
 180    quired for the STP. As a result, the inclusion of the STP does  
 181    not necessitate additional dispersion computations. The back-  
 182    ward dispersion plume results represent the sensitivity of the  
 183    plume’s coverage of spatiotemporal coordinates to the recep-  
 184    tor. In other words, if a spatiotemporal coordinate represents  
 185    the real release source, the concentration detected at the cor-  
 186    responding receptor site can be expressed as:

187     $conc_{rec} = Q_{rel} \frac{s}{\Delta T v}$  (5)

188    where  $conc_{rec}$  is the concentration at the receptor site,  $Q_{rel}$   
 189    is the release from source,  $s$  is sensitivity to emission from  
 190    the source, and  $\Delta T, v$  represent the time interval and grid  
 191    volume of simulation, respectively. Clearly, when a concen-  
 192    tration of radioactive contaminants is obtained at a receptor  
 193    site ( $conc_{rec} \neq 0$ ), the source must be within the coverage of  
 194    the backward plume ( $s \neq 0$ ). Conversely, when concentration  
 195    is not detected at a receptor site ( $conc_{rec} = 0$ ), the releasing  
 196    source ( $Q_{rel} \neq 0$ ) must be outside the coverage of backward  
 197    plume ( $s = 0$ ).

198    Based on the above logic, we extract prior information  
 199    from backward plumes. For each backward plume matrix  
 200    (hereafter referred to as  $BPM$ , it is a three-dimensional ma-  
 201    trix that stores the results of backward dispersion sensitivity),  
 202    the sensitivity to emission decreases sharply with increasing  
 203    diffusion distance, usually differing by several orders of mag-  
 204    nitude. Therefore, in this study, we characterize the backward  
 205    plume at receptor sites with detection values using weights  $K$ ,  
 206    and define the following spatiotemporal trajectory matrix:

207     $M_{>0}(\mathbf{x}_i, t) = \sum_{i=1}^{N_{>0}} K \text{ if } BPM_i(\mathbf{x}_i, t) \neq 0$  (6)

208    where  $N_{>0}$  is number of receptors with non-zero mea-  
 209    surements.

210    In the early stages of an accident, there are typically only  
 211    a few detections at selected receptors, while the majority of  
 212    receptors have no detections. However, this part of the infor-  
 213    mation is still of great value. Considering the detection limit  
 214    of the detection equipment in practice, it may not be possible  
 215    to detect very low concentrations of radioactive contaminants.  
 216    Therefore, the possibility that the spatiotemporal coordinates  
 217    covered by backward plumes of non-detected receptors can-  
 218    not be completely ruled out must be acknowledged. After  
 219    considering non-detection receptors, we correct spatiotempo-  
 220    ral trajectory matrix as:

221     $M_{ST} = \lambda \circ M_{>0}$  (7)

222    
$$\lambda(x_i, t) = 1 - \frac{\sum_{j=1}^{N_0} 1 \text{ if } BPM_j(\mathbf{x}_j, t) \neq 0}{N_0}$$
 (8)

223    where  $N_0$  is the number of non-detection receptors,  $\circ$  repre-  
 224    sents Hadmard product.

225    The source is necessarily located in the spatiotemporal re-  
 226    gion where the backward trajectories overlap most signifi-  
 227    cantly. We define the temporal prior as:

228     $P_t(t) = \text{normalize}(\max_x M_{ST}(x, t))$  (9)

229    Here, *normalize* refers to the process of adjusting the prob-  
 230    ability density so that its integral equals one.

231    Since the solution variables in our work are the start time  
 232    and the end time, the corresponding prior distributions are  
 233    treated as follows:

234    
$$P(t_s) \cdot P(t_e) = \frac{\sum_{t \in [t_s, t_e]} p_t(t)}{\max(p_t(t)) \cdot (t_e - t_s)}$$
 (10)

235    Similarly, we define the spatial prior, but considering that  
 236    the extent of the backward plume gradually increases with  
 237    diffusion time—leading to significant artifacts in the spatial  
 238    prior—we weight it using the temporal prior function:

239     $P_s(x) = \text{normalize}(\max_t (M_{ST}(x, t) \cdot P_t(t)))$  (11)

240    For the choice of  $K$ , we have two approaches: 1) the adop-  
 241    tion of uniform weights, and 2) weighting with the detec-  
 242    tion values of receptors. The information corresponding to  
 243    method 2 is implicit in the intrinsic properties of likelihood  
 244    function. Therefore, method 1 is chosen in this work to ob-  
 245    tain additional trajectory overlap information, which further  
 246    constrains the Bayesian inversion method. The spatiotempo-  
 247    ral prior effectively identifies the high-probability density re-  
 248    gions of the source term in both time and space, and it has  
 249    been shown to align well with the true source term (see sec-  
 250    tion III A 1 for details). Notably, the spatiotemporal prior can  
 251    be generalized to nearly all inversion methods, as it quickly  
 252    determines approximate information about the source term.

253    For total release quantity  $Q$ , given that the range of values  
 254    may span multiple orders of magnitude, the logarithm of  $Q$  is  
 255    assumed to follow a uniform distribution. Saunier et al.[18]

257 demonstrated that the diagonal matrix assumption is justified  
 258 for detections that are far apart, meaning the detections are  
 259 independent of each other. For the sake of simplification in  
 260 calculations, we assume that the accuracy of the detecting in-  
 261 struments is comparable, thus supporting the homoscedastic-  
 262 ity assumption ( $\mathbf{R} = \mathbf{I}_r$ ) . In this work, we assume that  $r$   
 263 follows a uniform distribution over a specified range (0.01-  
 264 20).

## 265 2. Likelihood

266 Likelihood is a quantitative description of the probability  
 267 of detections given a source term. Specifically, it is a func-  
 268 tion that quantifies the difference between the vector of de-  
 269 tected values  $\mathbf{Y}_{\text{det}}$  and the vector of simulated values  $\widehat{\mathbf{Y}}$  of  
 270 the source term to be determined.

271 Dumont Le Brazidec et al.[26] compared the performance  
 272 of different likelihood functions and points out that the choice  
 273 of likelihood function significantly impacts the performance  
 274 of the inversion model. Referring to previous studies, the log-  
 275 normal distribution may be the better choice for a likelihood  
 276 function:

$$277 P(\widehat{\mathbf{Y}}|\mathbf{X}) = \frac{e^{-\frac{1}{2} \ln(\frac{\widehat{\mathbf{Y}}_{\text{det}}}{\widehat{\mathbf{Y}}})^T \mathbf{R}^{-1} \ln(\frac{\widehat{\mathbf{Y}}_{\text{det}}}{\widehat{\mathbf{Y}}})}}{\sqrt{(2\pi)^{N_{\text{det}}} |\mathbf{R}|^{1/2} \prod_{i=1}^{N_{\text{det}}} y_i}} \quad (12)$$

278 where  $N_{\text{det}} = N_{>0} + N_0$  and  $\widehat{\mathbf{Y}}$  is calculated from eq.1 i.e.  
 279  $\widehat{\mathbf{Y}} = \mathbf{H}\mathbf{X}$ . This study utilizes many zero-value detections  
 280 (detections under detection limit), which fall outside the do-  
 281 main of definition for the logarithm. Therefore, we set a trun-  
 282 cation threshold, as in the work of Liu et al.[44] and define a  
 283 function in place of the logarithmic function in eq.12:

$$284 \zeta(y) = \ln\left(\frac{y + \theta}{y_{\text{ref}}}\right) \quad (13)$$

285 where  $y_{\text{ref}}$  is defined as reference concentration and  $y_{\text{ref}} =$   
 286  $2\theta = \min(y_i)$  which references the work of Dumont Le  
 287 Brazidec et al.[25].

## 288 C. Joint adaptive MCMC sampling

289 MCMC is a class of algorithms used to sample from  
 290 the probability distribution  $P(\mathbf{X}|\mathbf{Y})$ . The core idea is to  
 291 construct a Markov chain with the target distribution as its  
 292 equilibrium distribution. By simulating the Markov chain  
 293 and running it for a sufficient number of steps, the state of  
 294 the chain will eventually converge to the target distribution.  
 295 The Metropolis-Hastings (MH) algorithm is one of the most  
 296 widely used methods in MCMC, with its sampling efficiency  
 297 largely dependent on the choice of the transition proposal  
 298 function[23]. The adaptive transition proposal function ad-  
 299 dresses the issue of step size adaptation for arbitrarily com-  
 300 plex target distribution, but it also introduces non-Markovian

301 behavior into the sampling process. In this study, we pro-  
 302 posed a joint adaptive transition proposal (JATP) method to  
 303 mitigate this problem, ensuring robustness of the sampling  
 304 process. Specifically, we use three adaptive Metropolis pro-  
 305 posal functions: Adaptive Metropolis (AM)[45], Differential  
 306 Evolution-Markov Chain (DE-MC) algorithm[46], and Sin-  
 307 gle Component Adaptive Metropolis (SCAM)[47], propor-  
 308 tionally in the sampling process. In practice (see section  
 309 III A 2 for details), this method ensures that the converged  
 310 acceptance rate approaches the theoretically derived optimal  
 311 rate (approximately 0.234) for 1-10 dimensional cases, as  
 312 suggested by Roberts et al.[48].

313 When sampling high-dimensional probability density func-  
 314 tions, MCMC is often combined with parallel tempering (PT)  
 315 algorithms to balance local characterization and global ex-  
 316 ploration. [49]. The choice of temperature schedule is criti-  
 317 cal. Many of the previous studies suggested that a geometric  
 318 spacing was optimal[49], therefore, in this work, we simi-  
 319 larly choose geometric spacing and investigate the optimal  
 320 temperature schedule (see section III A 3 for details) selec-  
 321 tion in the source term inversion problem. We finalized the  
 322 temperature schedule using 8 Markov chains with different  
 323 temperatures, following a geometric progression. The rate  $\lambda$   
 324 is set to the natural logarithm base  $e$ , such that  $T_{i+1} = \lambda T_i$ ,  
 325 where  $i = 1, 2, \dots, 7$ , with  $T_1 = 1$  and  $T_8 = e^7 \approx 1097$ .  
 326 Inter-chain exchanges are performed every 100 steps.

## 327 D. Evaluation methodology

### 328 1. Evaluation metrics

329 1. *source inversion*. Relative errors in position ( $\delta_x$ ) total  
 330 release ( $\delta_Q$ ) and total relative errors ( $\delta_{\text{total}}$ ) are defined  
 331 to assess the accuracy of the reconstructed source terms  
 332 and the reliability of the method:

$$333 \delta_x = \frac{|\mathbf{x}_{\text{true}} - \mathbf{x}_{\text{rec}}|}{L} \times 100\% \quad (14)$$

$$335 \delta_Q = \frac{|Q_{\text{true}} - Q_{\text{rec}}|}{Q_{\text{true}}} \times 100\% \quad (15)$$

$$336 \delta_{\text{total}} = \sqrt{\delta_x^2 + \delta_Q^2} \times 100\% \quad (16)$$

337 where  $\mathbf{x}_{\text{true}}$  and  $Q_{\text{true}}$  represent the position and to-  
 338 tal release of the real source term, respectively, while  
 339  $\mathbf{x}_{\text{rec}}$  and  $Q_{\text{rec}}$  represent the position and total release  
 340 of the reconstructed source term.  $L$  denotes the char-  
 341 acteristic length of the simulation domain (the longer  
 342 boundary of the experimental domain is used). The to-  
 343 tal relative error is the  $L_2$  paradigm of each error com-  
 344 ponent. Since it is difficult to accurately measure the  
 345 inversion accuracy of the source item nuclide release  
 346 time intervals by the statistical values of the release  
 347 start and end times, only individual inversion cases are  
 348 illustrated without setting statistical metrics.

350    2. *Jensen-Shannon (JS) divergence.* JS divergence is a  
 351    common measure of the similarity between two prob-  
 352    ability density distributions[50] and is defined as fol-  
 353    lows:

354     $D_{JS}P||Q = \frac{1}{2}D_{KL}(P||M) + \frac{1}{2}D_{KL}(Q||M)$     (17)

356     $D_{KL}(P||Q) = \sum_i P(i) \log \frac{P(i)}{Q(i)}$     (18)

357    where  $M$  is the mean distribution of the distributions  $P$   
 358    and  $Q$ , i.e.,  $M = \frac{1}{2}(P+Q)$ . The value of JS divergence  
 359    is in the range of  $[0, 1]$ , the closer the JS divergence  
 360    is to 0 the more similar the two distributions are, and  
 361    conversely, the further from 0, the more different they  
 362    are.

## 363    2. Statistical method

364    The bootstrap method was employed for statistical vali-  
 365    dation of the effectiveness of the proposed approach. It is a com-  
 366    putationally convenient statistic (parameter estimation or sta-  
 367    tistical inference for sample sets with multiple repetitive sam-  
 368    pling) that does not depend on assumptions about the form of  
 369    the distribution or the variance, and remains valid for small  
 370    samples. It is much more accurate than classical inferences  
 371    based on Normal or t distributions in many cases.

## 372    3. Validation experiment

373    The proposed method utilizes the ETEX-I field experiment  
 374    as a benchmark for optimization and validation.

375    The ETEX-I experiment, conducted from October to  
 376    November 1994, was an atmospheric tracer study organized  
 377    by several European countries, involving a total of thirty-six  
 378    organizations worldwide[33]. The experiment involved a uni-  
 379    form tracer release at Monterfil in Brittany, France ( $48.058^\circ$   
 380    N,  $2.0083^\circ$  W), occurring from 16:00 UTC on October 23 to  
 381    03:50 UTC on October 24. During this release period, a total  
 382    of 340 kg of PMCH was emitted into the atmosphere. The  
 383    experiment yielded 3,104 detections from 168 ground sites,  
 384    with each data representing a three-hour average concentra-  
 385    tion. The release position and the locations of the ground  
 386    sites are shown in Fig. 1a.

## 387    4. Settings of validation schemes

388    1. *fixed-sites validation experiment.* Detecting data from  
 389    a randomly selected set of ground stations (B03, F03,  
 390    N01, R02) was utilized to optimize the joint adaptive  
 391    MCMC sampling method, specifically for hyperparam-  
 392    eter selection. The positions and labels of the selected  
 393    stations are depicted in Fig. 1b. For the JAPT algo-  
 394    rithm, we separately conducted 50 iterative sampling

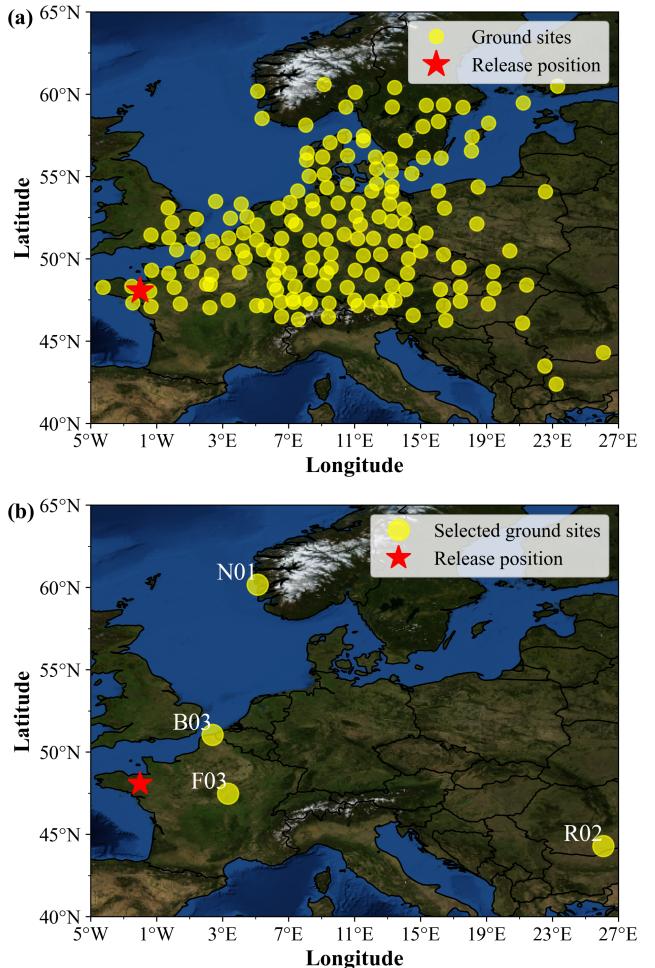


Fig. 1. Positions of release source and ground sites. The red star indicates the true source release position, while the yellow dots represent the positions of ground detection sites. (a) Positions of source and all ground sites in ETEX-I. (b) Positions of the randomly selected ground sites (B03, F03, N01, R02). The basemap is sourced from NASA's October Blue Marble Next Generation, featuring topography and bathymetry (<https://visibleearth.nasa.gov/collection/1484/blue-marble>).

395    calculations using AM, DE-MC, and SCAM individ-  
 396    ually, comparing the acceptance rate curves of each  
 397    scheme to determine the weight ratio of the basic algo-  
 398    rithms in the joint adaptive approach. For the tem-  
 399    perature schedule of the PT algorithm, we compared dif-  
 400    ferent temperature schemes based on their burn-in peri-  
 401    ods to identify the relatively optimal configuration. The  
 402    joint adaptive MCMC sampling method, with these op-  
 403    timized hyperparameters, was then applied to subse-  
 404    quent source term inversion calculations.

405    2. *statistical validation experiment.* Using the bootstrap  
 406    method, random sampling with replacement was con-  
 407    ducted from all detecting data of ETEX-I to explore the  
 408    properties of STP. Taking the STP generated from the  
 409    full dataset as a reference, the sensitivity of STP to data

volume is assessed through a comparison of JS divergence. Based on these results, the required data volume for inversion calculations is determined, enabling a statistical analysis of the improvements introduced by the STP algorithm to the inversion problem.

3. *ideal twin experiment.* In practical cases, it is challenging to estimate the errors in input data. Therefore, using the release scenario from ETEX-I, model simulation results are treated as true concentration values. By introducing relative errors, a twin experiment is designed to investigate the sensitivity of the Bayesian inversion method based on STP to input data errors under complex scenarios.

### III. RESULTS AND DISCUSSION

#### A. Hyperparameter optimization for joint adaptive MCMC method

##### 1. The inversion performance of fixed-sites scheme

Table 1 compares the inversion results of the fixed-sites scheme used for parameter optimization with the true source term, revealing that the inversion results are quite good, with a location error of 0.5% (15.71 km) and a relative error of 26% for the release quantity. While this result is generally satisfactory, the inversion of the release time indicates that, although the end time is accurately reconstructed, the start time is relatively earlier. This trend aligns with the temporal prior and is a consequence of the backward dispersion of the "plume" (described in Section 3.2.1).

##### 2. Weight selection for JATP algorithm

Through comparative testing, we determined the optimal mixing ratio ( $DE:AM:SCAM = 0.56:0.22:0.22$ ) of the three adaptive transition proposal algorithms. As shown in Fig. 2, the acceptance rate of the DE algorithm gradually increases with the number of iterations, stabilizing around 0.3—higher than the optimal acceptance rate. In contrast, the acceptance rates for the AM and SCAM algorithms gradually decrease, converging to 0.06 and 0.19, respectively, ultimately stabilizing at rates lower than optimal. Notably, the joint adaptive transition proposal algorithm mitigates the non-Markovian nature introduced by the historical trajectories of single adaptive approaches, ensuring that the acceptance rate remains near the theoretical optimum throughout the process, even from the early stages of iteration. This indicates that the JATP algorithm achieves an optimal match between step size and the geometric characteristics of the high-dimensional target distribution, thereby attaining superior sampling efficiency[48].

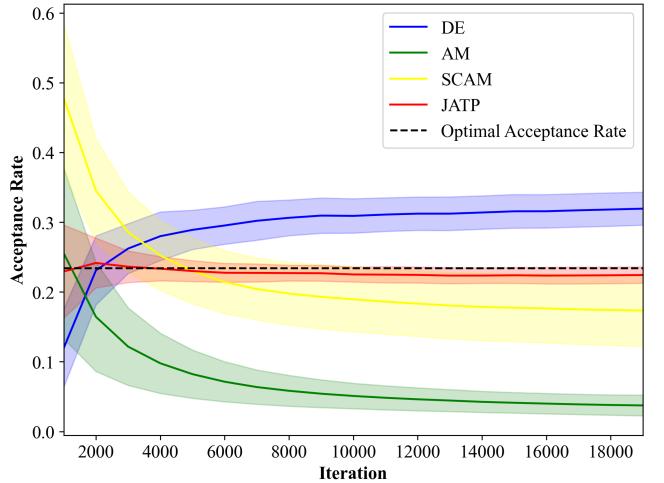


Fig. 2. Curves depicting the acceptance rates against the number of iterations for various adaptive transition proposal algorithms, based on 80 runs. The solid lines represent the average acceptance rates every 50 iterations for each algorithm, while the dashed line indicates the optimal acceptance rate (0.234). The shaded areas represent one standard deviation around the mean.

##### 3. Temperature schedule of PT algorithm

Fig. A.1 illustrates the convergence curves of source term variables from multiple runs with varying numbers of tempering chains, all maintained at a fixed geometric spacing  $e$ . While all curves converge near the true value, the convergence iterations for the parallel tempering MCMC occur significantly earlier than those of the classical single-chain MCMC. Furthermore, as the number of chains increases, the iterations for variable convergence consistently occur earlier. Notably, unstable convergence was observed at  $n = 5$ , which may be attributed to the intrinsic properties of the sampled distribution. Fig. 3(a) presents the average burn-in period for each temperature schedule under these conditions. It is evident that after  $n = 3$  (i.e., two tempering chains with a maximum temperature of  $e^2$ ), the rate of convergence stabilizes. Figs. A.2 and A.3 display the trace plots for multiple sampling calculations with a fixed number of chains ( $n = 3$ ) and a fixed maximum temperature ( $T_{\max} = e^2$ ), respectively. Figs. 3(b) and 3(c) show the corresponding average burn-in period variation curves. As illustrated in Fig. 3(b), when the number of chains is fixed, an increase in geometric spacing initially causes a decrease in the convergence position or iteration of the variable, followed by an increase. The optimal geometric spacing is observed at  $e \sim 3.2$ , as excessive geometric spacing ( $> 3.2$ ) can hinder exchanges between adjacent chains, leading to insufficient exploration of the solution space by the low-temperature Markov chain and difficulty in escaping local extrema. Conversely, if the geometric spacing is too small ( $< e$ ), although chain exchanges occur more frequently, the relatively low maximum temperature fails to fully leverage the global search capability of the high-temperature chains. This results in minimal gains from

Table 1. Source inversion result and relative errors for selected ground sites (B03, N01, F03, R02).  $\mathbf{X}_{rec}$  and  $\mathbf{X}_{real}$  stand for the inversion result and the true source term, respectively.

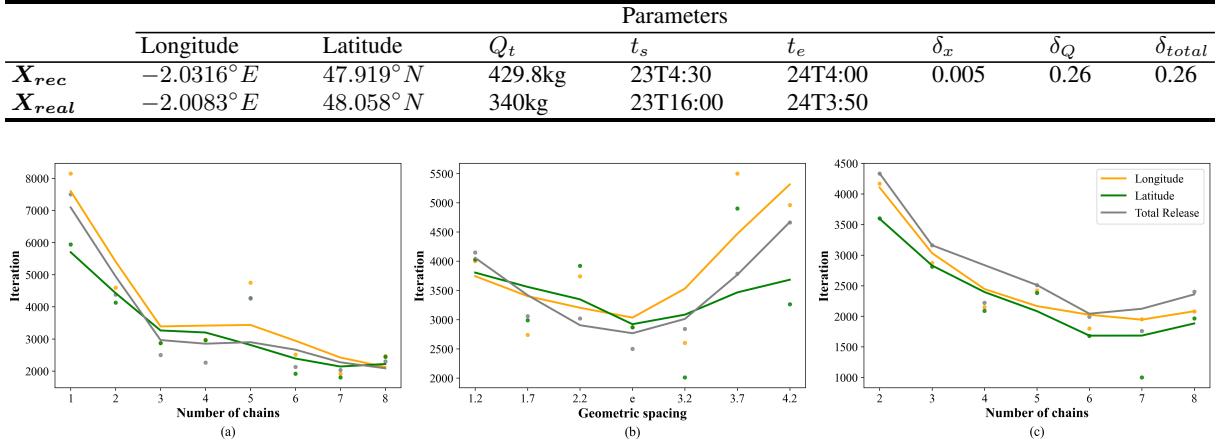


Fig. 3. LOWESS regression curves of the average burn-in period under various temperature schedules. (a) The geometric spacing is fixed at  $e$ ; (b) The number of parallel chains is fixed at 3; (c) The maximum temperature is fixed at  $e^2$ .

each exchange while adding computational burden without significantly enhancing exploration performance. Fig. 3(c) demonstrates that, with a fixed maximum temperature, the number of iterations required for convergence decreases as the number of chains increases. However, once the number of chains reaches 4 or more, the convergence iterations tend to stabilize. This indicates that when the maximum temperature is fixed, as long as the geometric spacing between adjacent annealing chains meets the exchange requirements, the sampling performance of the Markov chain will remain consistent. Based on simulation comparisons, the geometric spacing of MCMC sampling in our inversion problem should be between  $e$  and 3.2, with the maximum temperature exceeding  $e^2$ . Consequently, we selected a temperature schedule featuring 8 chains (7 tempering chains) with a geometric spacing of  $e$  and a maximum temperature of  $1097(e^7)$ . This schedule resulted in an approximate 2.89-fold improvement in convergence speed compared to the single-chain MCMC method.

## B. Source inversion based on STP

Fig. 4 presents the prior probability density distribution of the STP, derived from the all ground-based detection data collected during the ETEX-I experiment. To enhance clarity, we have excluded the negligible probability segments (those below a specified threshold  $1e^{-6}$ ) in the spatial probability density plot Fig. 4a. Notably, the true source position—indicated by a star symbol in Fig. 4a—and the actual release time, represented by the interval between the vertical lines in Fig. 4b, align closely within the region of maximum STP, reinforcing the robustness of our method for characterizing the source term. However, we observe a tendency for the region of maximum prior probability density to shift to an earlier position

(west of the source in Fig. 4a, aligned with the mean prevailing wind direction from west to east), and a similar pattern is evident in Fig. 4b. This shift arises from the sensitivity computations in the SRSM, which fundamentally follows a backward diffusion process. As the plume expands gradually during the diffusion, the decay of plume overlap becomes slow after reaching an extreme value. This gradual decay results in an artifact of elevated probability density in the STP estimation during earlier moments. Nevertheless, this effect does not compromise the validity of the method, as detailed in section III B 2. Fig. 5 illustrates the impact of using the temporal prior to weight the spatial prior, as mentioned in section II B 1. After applying the temporal prior to the spatial prior (Fig. 5b), it becomes clear that the distribution of probability densities is more concentrated around the actual release source compared to the unweighted distribution (Fig. 5a). As shown in Fig. 5c, the significance of the temporal weighting lies in its ability to increase the probability density near the true source while decreasing it in other regions, which, according to eq.3, effectively modifies the posterior probability density distribution.

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### 1. Effectiveness of STP

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### 2. Sensitivity of STP to data volume

Fig. 6 illustrates the distribution of JS divergence between the STP computed with varying numbers (10, 20, 30, 40, 50, and 60) of detections and the STP derived from the full dataset. For each data volume, 300 ( $3104/10 \approx 300$ ) independent computations were performed. The JS divergence of the spatial prior distribution is slightly higher than that of the temporal prior distribution. This discrepancy arises because different site selections lead to variations in the backward plume release positions, resulting in differences in the spatial prior distribution, particularly near the chosen sites. However, this effect diminishes closer to the source as the

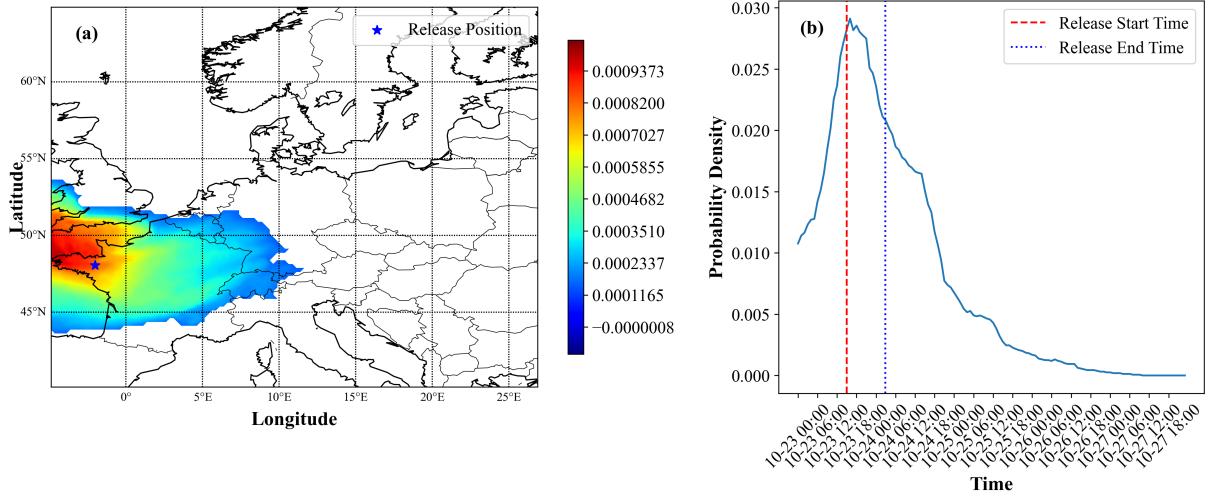


Fig. 4. STP probability density distribution derived from all detections. (a) Spatial probability density distribution; (b) Temporal probability density distribution.

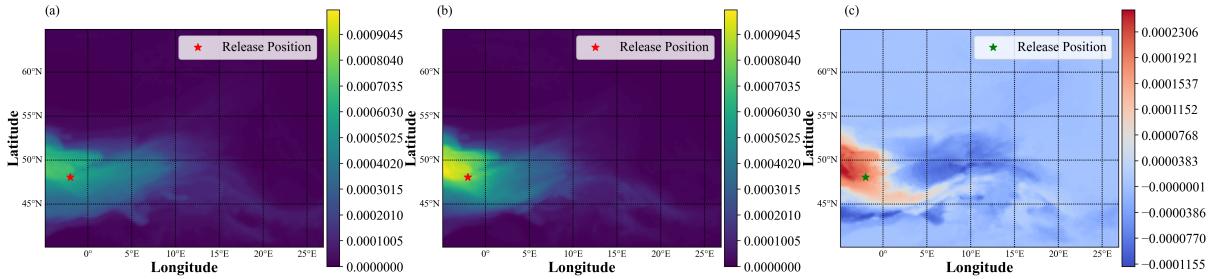


Fig. 5. Impact of temporal prior weighting on spatial prior. (a) Spatial prior unweighted by temporal prior. (b) Spatial prior weighted by temporal prior. (c) Comparison of changes before and after weighting.

553 plume develops over time. In contrast, the sensitivity to emis-  
 554 sions represented by the backward plumes is maximized at  
 555 the release time due to the uniqueness of the actual release  
 556 source, leading to much less variation in the temporal prior.  
 557 Consequently, the mean JS divergence lies between the two  
 558 distributions. As the number of detections increases, the in-  
 559 terquartile range (IQR) of JS divergence remains below 0.1  
 560 when the data volume exceeds 30. As the number of detec-  
 561 tions increases, the interquartile range (IQR) of JS divergence  
 562 remains below 0.1 when the data volume exceeds 30, indi-  
 563 cating that STP demonstrates robust performance in estimat-  
 564 ing the source term distribution even with a limited quantity  
 565 of detection data. In this study, considering the scarcity of  
 566 real-scenario detections and the need for the prior function to  
 567 be as accurate as possible, we set the number of detections  
 568 for each subsequent computational simulation at 40. Con-  
 569 sequently, the number of independent computations used for  
 570 statistical analysis was 80 ( $3104/40 \approx 80$ ).

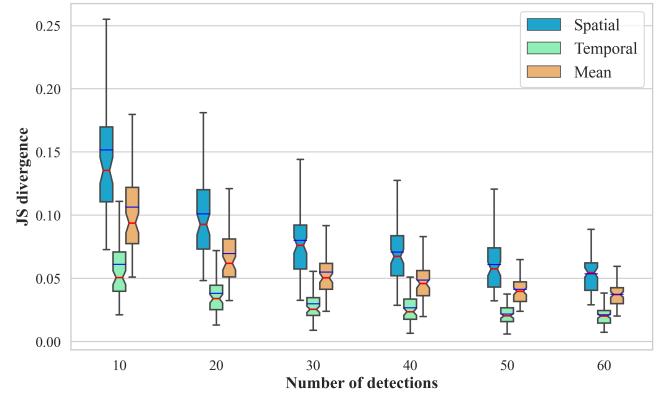


Fig. 6. Sensitivity of the spatiotemporal trajectory prior to site se-  
 lection and data volume. The red solid line represents the median  
 JS divergence, while the blue solid line indicates the mean JS diver-  
 gence. The upper and lower boundaries correspond to the upper and  
 lower quartiles, respectively. The whiskers extend to 1.5 times the  
 interquartile range (IQR).

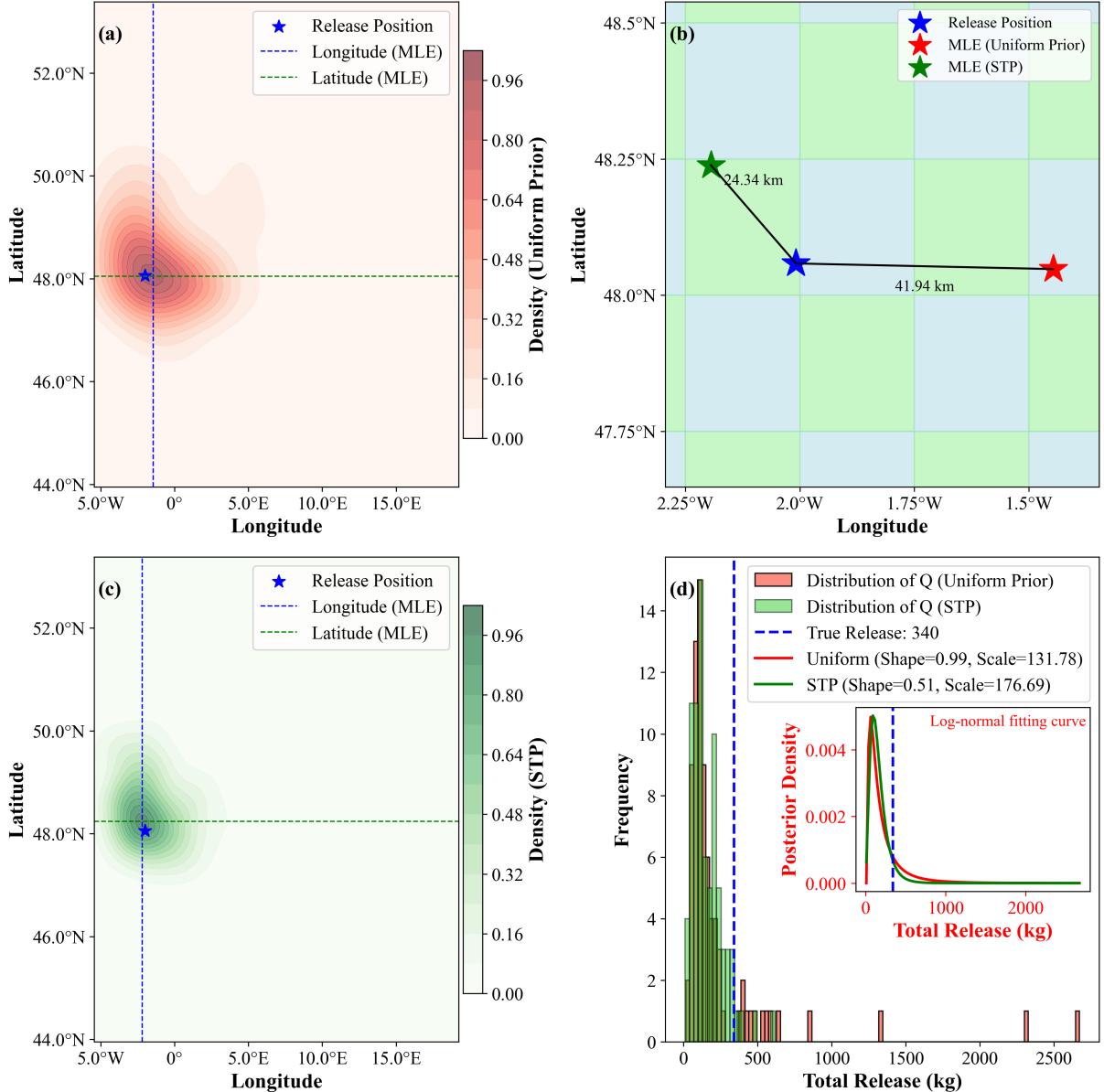


Fig. 7. Result's distribution of uniform prior and STP inversion after 80 runs. (a) Spatial distribution of inversion results based on the uniform prior. (b) Maximum likelihood estimation (MLE) of spatial distributions for uniform prior and STP inversion results, the grid represents the minimum resolution grid ( $0.25^\circ$ ) used in the dispersion simulation. (c) Spatial distribution of STP inversion results. (d) Inversion total release distributions for uniform prior and STP.

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### 3. Statistical evaluation of inversion results

573 A comparison of Fig. 7a and 7c clearly reveals that the  
 574 source positions obtained through STP inversion are more  
 575 concentrated around the true source positions. Furthermore,  
 576 Fig 7b illustrates the relative positions of the maximum likeli-  
 577 hood estimates (MLE) of the inversion results for the uniform  
 578 prior and STP, in comparison with the true release locations.  
 579 It is evident that the relative distance between the MLE of  
 580 STP and the true release location is significantly smaller than  
 581 that for the uniform prior. Notably, the MLE obtained with  
 582 STP lies within the same minimum resolution grid ( $0.25^\circ$ ) as

583 the true release location. Fig. 7d illustrates the distribution of  
 584 total release in the inversion results under two different prior  
 585 conditions. It is evident that both priors underestimate the  
 586 true release quantity, likely due to systematic biases in the in-  
 587 put data. However, a closer examination of the distributions  
 588 reveals a stark contrast: the inversion results with the uni-  
 589 form prior display numerous extreme values, with many in-  
 590 version results significantly exceeding the true release quan-  
 591 tity, despite the overall inversion being smaller. This sug-  
 592 gests that using the traditional uniform prior is highly prone  
 593 to instability in the inversion process. In contrast, the STP-  
 594 based inversion results are more concentrated, with a notably

higher frequency near the true value. Since the prior distribution assumes that the release quantity follow a log-normal distribution, the results are fitted using a log-normal distribution. The STP inversion results are indeed more concentrated (with a smaller shape value) and closer to the true values (with a larger scale). Fig 8 illustrates the statistical distribution of relative errors in source inversion for the ETEX-I experiment, comparing the Bayesian method based on a STP with the traditional Bayesian method that employs a uniform prior. It is evident that the three types of relative errors in the STP inversion results are all smaller than those of the uniform prior. Specifically, the mean values (blue line) of the position relative error, total release relative error, and total relative error have been reduced by 25.9%, 27.7%, and 27.8%, respectively. The above results clearly demonstrate that STP effectively constrains the variance of the inversion results while enhancing their accuracy.

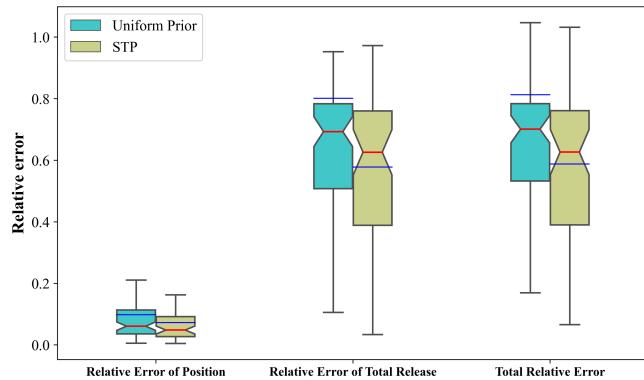


Fig. 8. Relative error distribution of source inversion results for ETEX-I experiment. The blue line represents the mean, while the red line denotes the median. The upper and lower boundaries correspond to the upper and lower quartiles, respectively. The whiskers extend to 1.5 times the interquartile range (IQR).

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#### 4. Sensitivity of STP to the relative errors

It is evident from Fig 9 that STP consistently outperforms the uniform prior in providing more concentrated and accurate location estimates under varying input data errors. Furthermore, as the input errors gradually increase, this "correction" effect does not show any signs of diminishing. Fig 10 presents a comparison of the relative errors in position, relative errors in total release, and total relative error under these conditions, with trends mirroring those in Figure 8. It is noteworthy that even in the absence of any input data errors, STP still demonstrates significantly better inversion results than the uniform prior. This indicates that the additional information introduced by STP compensates for the deficiencies in information utilization inherent in traditional methods, leading to a tangible improvement in inversion accuracy. In all cases, STP demonstrates superior inversion results. These results reveal STP's ability to limit the uncertainty in inversion outcomes caused by relative errors in the input data. This

ability provides more reliable source information under conditions where errors are difficult to estimate in real inversion scenarios, and such reliability can play a pivotal role in emergency decision-making.

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## IV. CONCLUSIONS

In this work, a Bayesian inversion method based on the backward plume spatiotemporal trajectory prior (STP) and joint adaptive MCMC sampling is proposed. The STP leverages fundamental fact that the backward plumes will overlap at the spatiotemporal coordinate of the release source, extracting prior information previously overlooked by traditional inversion methods from limited detection data, thereby enhancing both the accuracy and reliability of Bayesian inversion results. The joint adaptive MCMC sampling method introduces a Joint Adaptive Transition Proposal (JATP) to the conventional PT-based MCMC sampling. This approach addresses the challenge of designing transition proposals during sampling of high-dimensional complex objective functions, while also mitigating the non-Markovian nature of a single adaptive transition proposal. It strikes a better balance between global exploration and local characterization in the sampling process, ultimately improving sampling efficiency. Additionally, this paper investigates the optimal temperature schedule for the PT algorithm in the inversion problem, achieving faster convergence.

Subsequently, several inversion schemes based on the ETEX-I experiment were designed (fixed-sites validation experiment, statistical validation experiment, ideal twin experiment) to optimize and validate the proposed approach, while also investigating the sensitivity of the method to input data errors.

Firstly, the weights of the JATP were optimized. In the fixed-sites validation experiment, the acceptance rate curves for individual inversions using three adaptive transition proposal algorithms were compared to determine the optimal weight for the JATP. Verification showed that the weighted JATP consistently maintained an acceptance rate close to the theoretically derived optimal value (0.234) throughout the inversion iterations, thereby ensuring the efficiency of the sampling process.

Secondly, inversion calculations were performed using different temperature schedules in the fixed-sites validation experiment. The sensitivity relationships between the average burn-in period and the parameters of the PT algorithm's temperature schedule (number of chains, temperature intervals, and total temperature) were obtained, leading to the identification of the optimal temperature schedule for this method which reduced the average burn-in period by a factor of 2.89 compared to single-chain MCMC sampling.

Thirdly, using the complete ETEX-I experimental data, we qualitatively demonstrated the indicative effect of STP on the source term range, and quantitatively explored STP's sensitivity to data volume as well as its improvement effect on inversion results under the statistical validation experiment through the bootstrap method. The maximum probability

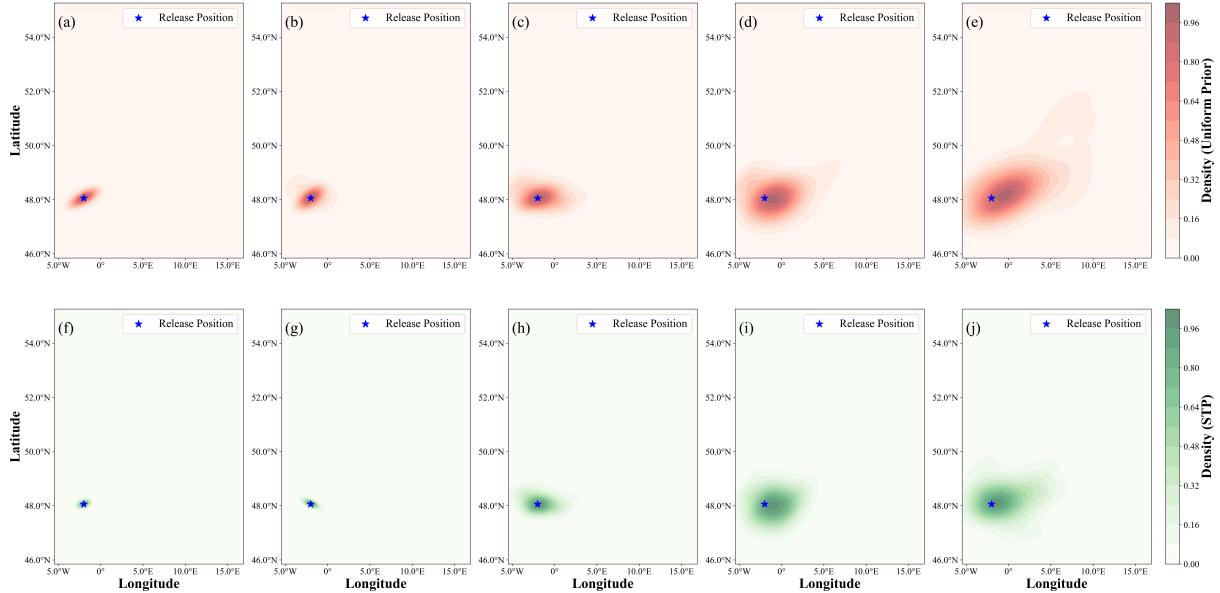


Fig. 9. Distribution of inversion source positions under varying levels of relative error. (a) and (b) represent 0% error, (c) and (d) represent 25% error, (e) and (f) represent 50% error, (g) and (h) represent 100% error, and (i) and (j) represent 200% error.

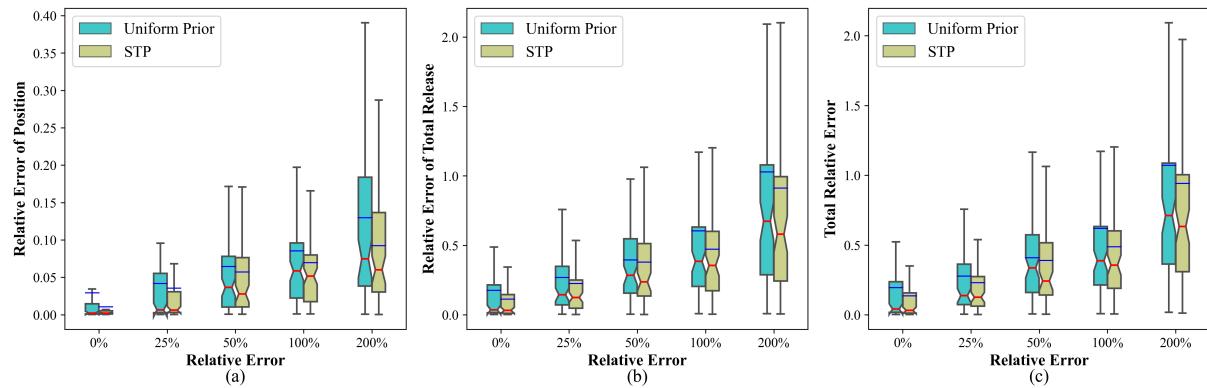


Fig. 10. The distribution of relative errors in the inversion results under different input data errors in the ideal twin experiment. (a) Relative error of position ( $\delta_x$ ); (b) Relative error of total release ( $\delta_Q$ ); (c) Total relative error ( $\delta_{total}$ ).

density region of STP can relatively accurately estimate the location and timing of the release before the inversion calculation. Moreover, STP exhibits relatively low sensitivity to data volume, showing effective indication when the data set exceeds 30 points. Incorporating STP into the inversion process significantly enhances the accuracy of the inversion results while constraining the uncertainty range, thus yielding more reliable outcomes. In the ETEX-I case, the mean relative errors in position, release quantity, and total error were reduced by 25.9%, 27.7%, and 27.8%, respectively, compared to the traditional uniform prior. Meanwhile, STP reduced the maximum likelihood estimate of the inversion position distribution to within the smallest resolution ( $0.25^\circ$ ) grid.

Finally, using the ideal twin experiment, we investigated STP's sensitivity to input data errors by introducing different relative errors. The results demonstrated that STP consistently produces more accurate inversion results and smaller

inversion error ranges under varying input data errors, with this improvement effect remaining strong even as the relative errors increase. It is also noteworthy that, even in the absence of any input data errors, STP still achieves higher inversion accuracy compared to the uniform prior.

These results indicate that, in practical scenarios, the optimized joint adaptive MCMC sampling and STP, when applied to Bayesian source inversion, can effectively enhance the inversion speed, accuracy, and robustness, thereby achieving satisfactory inversion results that meet the requirements of timeliness and accuracy in emergency decision-making. This method presents a promising solution for source inversion in atmospheric releases of radionuclides. However, the backward dispersion of the "plume" tends to cause the temporal prior to shift forward, resulting in an earlier inversion of the start time. Future work will focus on mitigating probability artifacts induced by dispersion to enhance the method further.

721    **Appendix A: Appendix A: Plots of the variable's sampling**  
722    **trajectories with different temperature schedules**

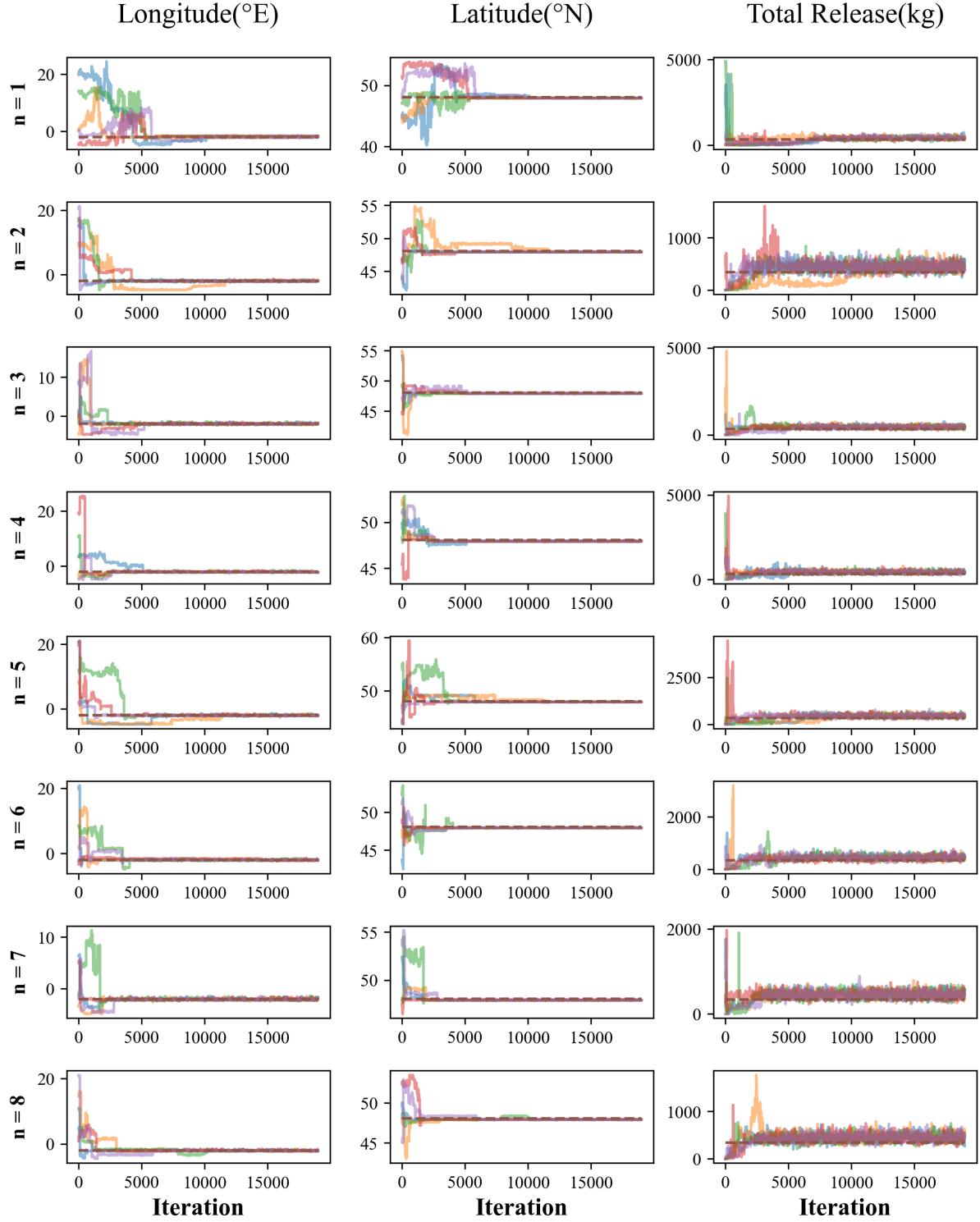


Fig. A.1. The sampling trajectories for the single-chain MCMC ( $n = 1$ ) and the parallel tempering algorithm MCMC ( $n = 2, 3, 4, 5, 6, 7, 8$ ) when the geometric spacing is  $e$ . The dashed line represents the true value of the variable and the solid lines represent the sampling curve.

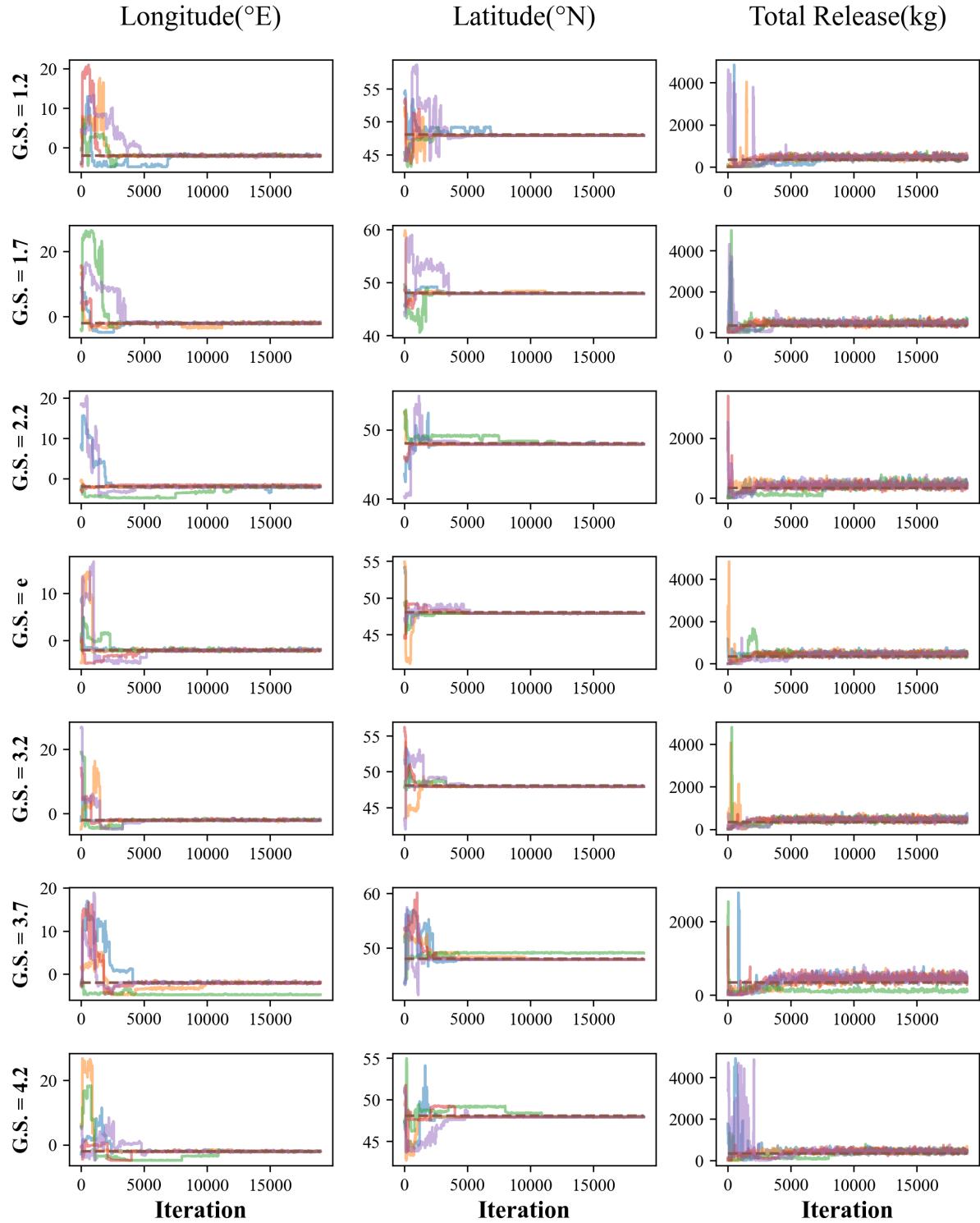


Fig. A.2. Plot of the variable's sampling trajectories at each geometric spacing (1.2, 1.7, 2.2,  $e$ , 3.2, 3.7, 4.2) with three chains. G. S. stands for geometric spacing.

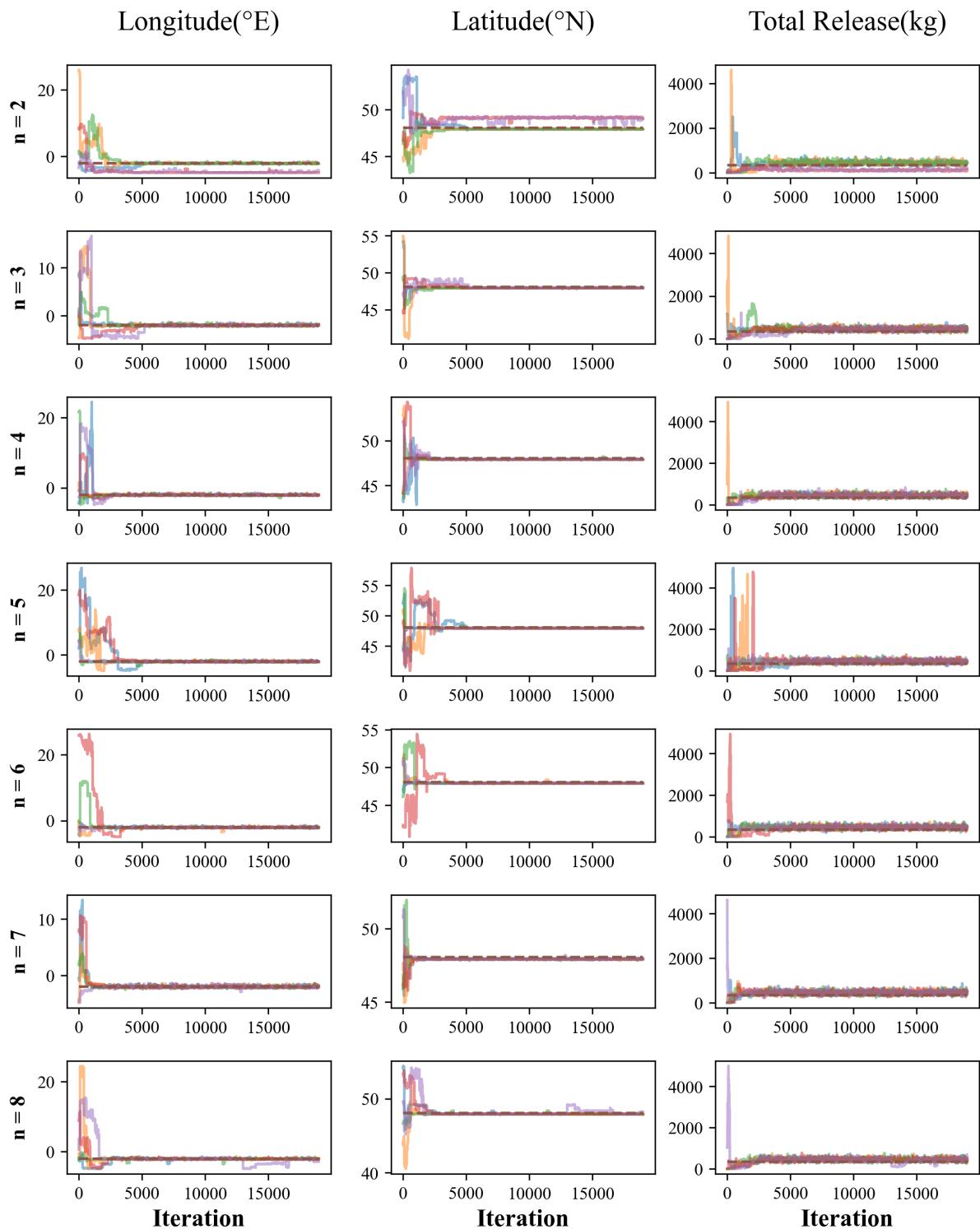


Fig. A.3. Plot of the variable's sampling trajectories at different chain numbers ( $n = 2, 3, 4, 5, 6, 7, 8$ ) with a maximum temperature of  $e^2$ .

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